AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A method for identifying and/or quantifying an organism or part of an organism in a sample by detecting a nucleotide sequence specific of said organism, wherein said specific nucleotide sequence presents a homology higher than 30% ~~60%~~ with at least 4 other homologous nucleotide sequences from other organisms comprising:

amplifying said specific nucleotide sequence by PCR into double-stranded target nucleotide sequence using primer pairs which are capable of amplifying at least two of said homologous nucleotide sequences from other organisms so as to produce a full-length target nucleotide sequence having between 100 and 800 bases;

contacting said target nucleotide sequence resulting from the amplifying step with single-stranded capture nucleotide sequences, said single-stranded capture nucleotide sequences being covalently bound in an array to an insoluble solid support via a spacer comprising a nucleotide sequence of at least 40 bases in length, wherein said array comprises at least 4 different bound single-stranded capture nucleotide sequences/cm^2 of solid support surface and wherein said capture nucleotide sequences comprise a nucleotide sequence of about 15 to about 40 bases which is able to specifically bind to said full-length target nucleotide sequence without binding to said at least 4 homologous nucleotide sequences; and

detecting specific hybridization of said target nucleotide sequence to said capture nucleotide sequences.

2. **(Previously presented)** The method according to claim 1, wherein the amplified nucleotide sequence is a DNA nucleotide sequence.

3. **(Canceled)**

4. **(Previously presented)** The method according to claim 1, wherein the amplified nucleotide sequences are mRNA first reverse transcribed into cDNA and then amplified using said primer pair which is capable of amplifying at least two of said homologous mRNA in said sample.

5-8. **(Canceled)**

9. **(Previously presented)** The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is more than about 10 fmoles per cm^2 of solid support surface.

10. **(Currently amended)** The method according to claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 60% ~~30%~~.

11. **(Canceled)**

12. **(Previously presented)** The method according to claim 1, wherein other primers are present-in the amplification step for the amplification of another nucleotide sequence.

13. **(Previously presented)** The method according to claim 1, wherein the insoluble solid support is selected from the group consisting of: glasses, electronic devices, silicon supports, plastic supports, compact discs, filters, filters, gel layers, and metallic supports.

14. **(Previously presented)** The method according to claim 1, wherein the nucleotide sequence to be identified and/or quantified is an RNA sequence submitted to a reverse transcription of its 3' or 5' end by using a consensus primer.

15. **(Previously presented)** The method according to claim 1, wherein the nucleotide sequence to be identified and/or quantified are from the *FemA* gene of Staphylococci species selected from the group consisting of: *S. aureus*, *S. epidermidis*, *S. saprophyticus*, *S. hominis* and *S. haemolyticus*.

16. **(Previously presented)** The method according to claim 1, wherein the solid support also bears capture nucleotide sequences specific of the homologous sequences specific for the binding with the homologous target nucleotide sequence together with a consensus sequence able to bind to said target nucleotide sequence and to said at least 4 homologous nucleotide sequences.

17. **(Original)** The method according to claim 1, wherein the solid support bears capture nucleotide sequences specific for the identification of two or more staphylococcus species together with a consensus sequence for a Staphylococcus genus identification.

18. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the *MAGE* gene family.

19. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the *HLA-A* genes family.

20. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the dopamine receptors coupled to the protein G genes family.

21. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the choline receptors coupled to the protein G genes family.

22. **(Previously presented)** The method according to claim 1, wherein the sequence to be detected and/or quantified in the sample belongs to the histamine receptors coupled to the protein G genes family.

23. **(Previously presented)** The method according to claim 1, wherein the sequence to be detected and/or quantified in the sample belongs to the cytochrome p450 forms family.

24. **(Withdrawn)** A diagnostic and/or quantification kit which comprises an insoluble solid support upon which single stranded capture nucleotide sequences are bound, said single stranded capture nucleotide sequences containing a sequence of between about 10 and about 60 bases specific for a target nucleotide sequence to be detected and/or quantified and having a total length comprised between about 30 and about 600 bases, said single stranded capture nucleotide sequences being disposed upon the surface of the solid support according to an array with a density of at least 4 single stranded capture nucleotide sequences/cm2 of the solid support surface.

25. **(Withdrawn)** The diagnostic kit according to claim 24, wherein the insoluble solid support is selected from the group consisting of glasses, electronic devices, silicon supports, plastic supports, compact discs, gel layers, metallic supports or a mixture thereof.

26. **(Withdrawn)** The diagnostic kit according to claim 24, wherein the capture nucleotide sequences are specific to a target nucleotide sequence to be detected and/or quantified which is specific for a gene selected from the group consisting of Staphylococcus species genes, MAGE genes family, HLA-genes family, dopamine, choline or histamine receptors coupled to the protein G genes family, cytochrome P450 forms family or GMO plants family.

27. **(Withdrawn)** The diagnostic kit according to claim 24, comprising biochips, for identification and/or quantification of 5 bacteria species obtained after amplification of one of their DNA sequences with one consensus primer(s) and detection on an array.

28. **(Withdrawn)** The diagnostic kit according to claim 24, comprising biochips, for identification and/or quantification of bacteria species together with the identification of the bacterial genus obtained after copying and/or amplification of one of their DNA or RNA sequences with one consensus primer(s) and detection on an array.

29. **(Withdrawn)** The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 15 Staphylococcus species obtained after copying and/or amplification of one of their DNA sequences with one consensus primer(s) and detection on an array.

30. **(Withdrawn)** The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more MAGE genes obtained after copying and/or amplification of one of their DNA or mRNA sequences with one consensus primer(s) and detection on an array.

31. **(Withdrawn)** The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more HLA-A sequences obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

32. **(Withdrawn)** The diagnostic kit according claim 24, comprising biochips, for detection and/or quantification of 3 or more gene sequences of receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

33. **(Withdrawn)** The diagnostic kit according to claim 32, comprising biochips, for detection and/or quantification of 3 or more gene sequences of dopamine receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

34. **(Withdrawn)** The diagnostic kit according to claim 32, comprising biochips, for detection and/or quantification of 3 or more gene sequences of serotonine receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

35. **(Withdrawn)** The diagnostic kit according to claim 32, comprising biochips, for detection and/or quantification of 3 or more gene sequences of histamine receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

36. **(Withdrawn)** The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more gene sequences of GMO plants obtained after

copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

37. **(Withdrawn)** The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more gene sequences the cytochrome P450 forms obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

38. **(Previously presented)** The method of Claim 1, wherein said nucleotide sequence to be identified and/or quantified originates from a microorganism.

39. **(Canceled)**

40. **(Previously presented)** The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is more than about 100 fmoles per cm^2 of solid support surface.

41. **(Canceled)**

42. **(Previously presented)** The method according to claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 80%.

43. **(Cancelled)**

44. **(Previously presented)** The method of Claim 12, wherein said other nucleotide sequence is an antibiotic resistance determining sequence.

45. **(Previously presented)** The method of Claim 1, wherein said organism is identified or quantitated by detecting a single spot signal at one specific location on said insoluble solid support.

SUMMARY OF INTERVIEW

Exhibits and/or Demonstrations

None

Identification of Claims Discussed

1, 2, 4, 9, 10, 12-23, 38, 40, 42, 44 and 45.

Identification of Prior Art Discussed

Guschin et al. (*Appl. Environ. Microbiol.* 1997 63:2397-2402)

Bamdad et al. (USP 6,541,617)

Proposed Amendments

Claim 1 was proposed to include the limitation which specifies that the target nucleotide sequence that is hybridized to the array-bound capture molecules is a full-length sequence of 100 to 800 bases.

Principal Arguments and Other Matters

1. The finality of the Office Action was discussed.

2. The inventor, Nathalie Zammatteo, described the claimed invention, and compared its features to the methods of the prior art references. Guschin et al. does not use full-length amplified sequences as target. Guschin clones PCR amplicons of approximately 1,500 bases and then expresses labeled RNA. The labeled RNA fragmented to pieces of approximately 40 bp in length are applied to the support. Guschin does not use a nucleotide spacer on the microchip support. Bamdad also uses a non-nucleotide spacer, long capture molecules (200-300 base pairs), and preferred distances from the support of 15-60 Å. Therefore, the method of the present invention is quite different of the cited references as it uses: short capture sequences (15-40 nucleotides), and requires direct labeling of the amplicons which are 100-800 bases long without prior fragmentation. Therefore, the cited references do not provide suggestion or motivation to modify the references to achieve the claimed invention, and do not teach or suggest all the claim limitations.

Results of Interview

1. The finality of the Office Action was discussed in view of the fact that no new amendments were made to the claims in the previous Office Action Response, but the new art was cited by the Examiner in the present Office Action. The Examiner agreed that the finality of

the Office Action was made by mistake and will be withdrawn. Thus, the response to the pending Office Action will be considered as an amendment after non-final.

2. The Examiner agreed to consider the proposed claim amendments and arguments, preferably supported by an Inventor's Declaration showing unexpected results using the claimed method.